

SEQUENCE LISTING

<110> Luo, Ying
 Xu, Xiang
 Rigel Pharmaceuticals, Inc.

<120> Novel TRAF4 Associated Cell Cycle Proteins,
 Compositions and Methods of Use

<130> 021044-004810US

<140> US 10/088,961

<141> Not yet assigned

<150> US 09/404,010

<151> 1999-09-23

<150> WO PCT/US00/40987

<151> 2000-09-25

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

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<223> cell cycle protein Mkinase

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 <213> Homo sapiens

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 35 40 45
 Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys Lys Ala Thr Gly Ser
 50 55 60
 Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro Gly Ala Glu Glu Gln
 65 70 75 80
 Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe Lys Thr Leu Arg His
 85 90 95
 Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu Thr Glu Lys Cys Leu
 100 105 110
 His Val Val Thr Glu Ala Val Thr Pro Leu Gly Ile Tyr Leu Lys Ala
 115 120 125
 Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu Ile Ser Trp Gly Leu
 130 135 140
 His Gln Ile Val Lys Ala Leu Ser Phe Leu Val Asn Asp Cys Ser Leu
 145 150 155 160

Ile His Asn Asn Val Cys Met Ala Ala Val Phe Val Asp Arg Ala Gly
165 170 175

Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr Ser Ala Gln Gly Asn
180 185 190

Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu Leu Glu Gln Tyr Asp
195 200 205

Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val Val Arg Glu Lys Trp
210 215 220

Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile Trp Glu Val Phe Asn
225 230 235 240

Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn Pro Gly Lys Ile Pro
245 250 255

Lys Thr Leu Ala Pro His Tyr Cys Glu Leu Val Gly Ala Asn Pro Lys
260 265 270

Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn Cys Arg Ala Pro Gly
275 280 285

Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn Leu Phe Leu Glu Glu
290 295 300

Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys Phe Phe Gln Glu Leu
305 310 315 320

Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe Cys Arg His Lys Leu
325 330 335

Leu Pro Gln Leu Leu Thr Ala Phe Glu Phe Gly Asn Ala Gly Ala Val
340 345 350

Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe Leu Ser Ala Glu Glu
355 360 365

Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys Met Phe Ser Ser Thr
370 375 380

Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln Met Glu Gln Phe Ile
385 390 395 400

Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln Ile Phe Pro His Val
405 410 415

Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile Arg Glu Gln Thr Val
420 425 430

Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn Glu Ala Asn Leu Asn
435 440 445

Val Glu Leu Met Lys His Phe Ala Arg Leu Gln Ala Lys Asp Glu Gln
450 455 460

Y Pro Ile Arg Cys Asn Thr Thr Val Cys Leu Gly Lys Ile Gly Ser
470 475 480

Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu Thr Ser Ala Phe Ser
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 Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met Asn Asp Cys Ala Gln
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 Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val Asp Pro Glu Lys Ser
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 Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu Glu Val Glu Lys Asp
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 Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu Thr Ser Lys Leu Ile
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 660 665 670
 Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu Ala Gln Gln Asp Asp
 675 680 685
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cyclin A
destruction box

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Arg Thr Val Leu Gly Val Ile Gly Asp
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<210> 4
<211> 9
<212> PRT
<213> Artificial Sequence

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destruction box

<400> 4
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<210> 5
<211> 27
<212> PRT
<213> Artificial Sequence

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destruction box

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Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
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Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
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<210> 6
<211> 28
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:mouse cyclin B
destruction box

<400> 6
 Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
 1 5 10 15

Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
 20 25

<210> 7
 <211> 27
 <212> PRT
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:mouse cyclin B1
 destruction box

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Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
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<210> 8
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 <212> PRT
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:mouse cyclin B2
 destruction box

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Val Gly Ile Thr Ala Leu Leu Leu Ala Ser Lys
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<210> 9
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse cyclin A2
 destruction box

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Leu Leu

<210> 10
 <211> 230
 <212> PRT
 <213> Artificial Sequence

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 AAA83272 and AAA947437 kinase "homologue" domain

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 20 25 30

Val Lys Leu Ala Lys His Val Ile Thr Gly His Glu Val Ala Ile Lys
 35 40 45

Ile Ile Asp Lys Thr Ala Leu Asn Pro Ser Ser Leu Gln Lys Leu Phe
 50 55 60

Arg Glu Val Lys Ile Met Lys Gln Leu Asp His Pro Asn Ile Val Lys
 65 70 75 80

Leu Tyr Gln Val Met Glu Thr Glu Gln Thr Leu Tyr Leu Val Leu Glu
 85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
 100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
 115 120 125

Val Gln Tyr Leu His Ser Lys Asn Ile Ile His Arg Asp Leu Lys Ala
 130 135 140

Glu Asn Leu Leu Leu Asp Gln Asp Met Asn Ile Lys Ile Ala Asp Phe
 145 150 155 160

Gly Phe Ser Asn Thr Phe Ser Leu Gly Asn Lys Leu Asp Thr Phe Cys
 165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Ser Gly Lys Lys Tyr
 180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
 195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
 210 215 220

Arg Glu Arg Val Leu Arg
 225 230

<210> 11
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 <212> PRT
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<223> Description of Artificial Sequence:GenBank
AAF72103/MAPK kinase "homologue" domain

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Gly Asn Tyr Arg Leu Gln Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
20 25 30

Val Lys Leu Ala Arg His Val Leu Thr Gly Arg Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Ile Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Tyr Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Leu Asp Gly Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
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Arg Glu Arg Val Leu Arg
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<210> 12

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:GenBank G01025
kinase "homologue" domain

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Val Lys Leu Ala Arg His Ile Leu Thr Gly Lys Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Ser Ser Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Val Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Phe Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Leu Asp Ala Asp Met Asn Ile Lys Ile Ala Asp Phe
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Gly Phe Ser Asn Glu Phe Thr Phe Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
210 215 220

Arg Glu Arg Val Leu Arg
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<223> Description of Artificial Sequence: GenBank P51954
Kinase "homologue" domain

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 35 40 45
 Arg Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val
 50 55 60
 Gln Tyr Lys Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met
 65 70 75 80
 Asp Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys
 85 90 95
 Gly Ala Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile
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 Cys Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp
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 Ile Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu
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 Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala
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 Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu
 165 170 175
 Asn Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val
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<210> 14

<211> 233

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Mkinase kinase
 "homologue" domain

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 20 25 30
 Arg Gly Arg Lys Lys Ala Thr Gly Ser Pro Val Ser Ile Phe Val Tyr
 35 40 45
 Asp Val Lys Pro Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Ala
 50 55 60

Phe Lys Arg Phe Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile
 65 70 75 80
 Asp Gly Leu Glu Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val
 85 90 95
 Thr Pro Leu Gly Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Gly Leu
 100 105 110
 Lys Glu Leu Glu Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu
 115 120 125
 Ser Phe Leu Val Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met
 130 135 140
 Ala Ala Val Phe Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu
 145 150 155 160
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 165 170 175
 Gly Ile Pro Glu Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser
 180 185 190
 Ser Gly Arg Val Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu
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 Ala Leu Arg Asn Pro Gly Lys Ile Pro
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<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:kinase
 "homologue" domain consensus peptide

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<210> 16

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:kinase
 "homologue" domain consensus peptide

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<210> 17
<211> 4
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:kinase
 "homologue" domain consensus peptide

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SEQUENCE LISTING

<110> Luo, Ying
 Xu, Xiang
 Rigel Pharmaceuticals, Inc.

<120> Novel TRAF4 Associated Cell Cycle Proteins,
 Compositions and Methods of Use

<130> 021044-004810US

<140> US 10/088,961
 <141> Not yet assigned

<150> US 09/404,010
 <151> 1999-09-23

<150> WO PCT/US00/40987
 <151> 2000-09-25

<160> 17

<170> PatentIn Ver. 2.1

<210> 1
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 <212> DNA
 <213> Homo sapiens

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 <223> cell cycle protein Mkinase

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atggaggcca aacgcgcgga gaggaaaggt gccaaaggcc ccatgaagct gggagccccg 2460
aaagctggat gaaccgtggc ggtggccctt cccggctgcg gagagcccgc cccacagatg 2520
tatttattgt acaaacaccatg tgagcccgcc cgggccagcc agggccatctc acgtgtacat 2580
aatcagagcc acaataaatt ctatttcaca aaaaaaaaaa aaaaaaaaaa aaaaaaacct 2640
cgag 2644

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<210> 2

<211> 831

<212> PRT

<213> Homo sapiens

<220>

<223> amino acid sequence which includes
cell cycle protein Mkinase

<400> 2

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Asn Ser Gly Asn Asn Ala Glu Glu Ala Pro Gly Ala Lys Ala Pro Glu
  1             5             10            15
Pro Ala Ala Ala Val Gly Thr Met Trp Phe Phe Ala Arg Asp Pro Val
          20             25            30
Arg Asp Phe Pro Phe Glu Leu Ile Pro Glu Pro Pro Glu Gly Gly Leu
          35             40            45
Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys Lys Ala Thr Gly Ser
          50             55            60
Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro Gly Ala Glu Glu Gln
          65             70            75            80
Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe Lys Thr Leu Arg His
          85             90            95
Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu Thr Glu Lys Cys Leu
          100            105            110
His Val Val Thr Glu Ala Val Thr Pro Leu Gly Ile Tyr Leu Lys Ala
          115            120            125
Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu Ile Ser Trp Gly Leu
          130            135            140
His Gln Ile Val Lys Ala Leu Ser Phe Leu Val Asn Asp Cys Ser Leu
          145            150            155            160

```

Ile His Asn Asn Val Cys Met Ala Ala Val Phe Val Asp Arg Ala Gly
 165 170 175
 Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr Ser Ala Gln Gly Asn
 180 185 190
 Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu Leu Glu Gln Tyr Asp
 195 200 205
 Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val Val Arg Glu Lys Trp
 210 215 220
 Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile Trp Glu Val Phe Asn
 225 230 235 240
 Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn Pro Gly Lys Ile Pro
 245 250 255
 Lys Thr Leu Ala Pro His Tyr Cys Glu Leu Val Gly Ala Asn Pro Lys
 260 265 270
 Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn Cys Arg Ala Pro Gly
 275 280 285
 Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn Leu Phe Leu Glu Glu
 290 295 300
 Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys Phe Phe Gln Glu Leu
 305 310 315 320
 Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe Cys Arg His Lys Leu
 325 330 335
 Leu Pro Gln Leu Leu Thr Ala Phe Glu Phe Gly Asn Ala Gly Ala Val
 340 345 350
 Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe Leu Ser Ala Glu Glu
 355 360 365
 Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys Met Phe Ser Ser Thr
 370 375 380
 Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln Met Glu Gln Phe Ile
 385 390 395 400
 Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln Ile Phe Pro His Val
 405 410 415
 Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile Arg Glu Gln Thr Val
 420 425 430
 Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn Glu Ala Asn Leu Asn
 435 440 445
 Val Glu Leu Met Lys His Phe Ala Arg Leu Gln Ala Lys Asp Glu Gln
 450 455 460
 Gly Pro Ile Arg Cys Asn Thr Thr Val Cys Leu Gly Lys Ile Gly Ser
 465 470 475 480

Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu Thr Ser Ala Phe Ser
 485 490 495
 Arg Ala Thr Arg Asp Pro Phe Ala Pro Ser Arg Val Ala Gly Val Leu
 500 505 510
 Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met Asn Asp Cys Ala Gln
 515 520 525
 Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val Asp Pro Glu Lys Ser
 530 535 540
 Val Arg Asp Gln Ala Phe Lys Ala Phe Arg Ser Phe Leu Ser Lys Leu
 545 550 555 560
 Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu Glu Val Glu Lys Asp
 565 570 575
 Val His Ala Ala Ser Ser Pro Gly Met Gly Gly Ala Ala Ala Ser Trp
 580 585 590
 Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu Thr Ser Lys Leu Ile
 595 600 605
 Arg Ser His Pro Thr Thr Ala Pro Thr Glu Thr Asn Ile Pro Gln Arg
 610 615 620
 Pro Thr Pro Glu Gly Val Pro Ala Pro Ala Pro Thr Pro Val Pro Ala
 625 630 635 640
 Thr Pro Thr Thr Ser Gly His Trp Glu Thr Gln Glu Glu Asp Lys Asp
 645 650 655
 Thr Ala Glu Asp Ser Ser Thr Ala Asp Arg Trp Asp Asp Glu Asp Trp
 660 665 670
 Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu Ala Gln Gln Asp Asp
 675 680 685
 Trp Ser Thr Gly Gly Gln Val Ser Arg Ala Ser Gln Val Ser Asn Ser
 690 695 700
 Asp His Lys Ser Ser Lys Ser Pro Glu Ser Asp Trp Ser Ser Trp Glu
 705 710 715 720
 Ala Glu Gly Ser Trp Glu Gln Gly Trp Gln Glu Pro Ser Ser Gln Glu
 725 730 735
 Pro Pro Ser Asp Gly Thr Arg Leu Ala Ser Glu Tyr Asn Trp Gly Gly
 740 745 750
 Pro Glu Ser Ser Asp Lys Gly Asp Pro Phe Ala Thr Leu Ser Ala Arg
 755 760 765
 Pro Ser Thr Gln Pro Arg Pro Asp Ser Trp Gly Glu Asp Asn Trp Glu
 770 775 780
 Gly Leu Glu Thr Asp Ser Arg Gln Val Lys Ala Glu Leu Ala Arg Lys
 785 790 795 800

<400> 6
 Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
 1 5 10 15
 Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
 20 25

<210> 7
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse cyclin B1
 destruction box

<400> 7
 Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg
 1 5 10 15
 Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
 20 25

<210> 8
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse cyclin B2
 destruction box

<400> 8
 Asp Arg Phe Leu Gln Ala Gln Leu Val Cys Arg Lys Lys Leu Gln Val
 1 5 10 15
 Val Gly Ile Thr Ala Leu Leu Leu Ala Ser Lys
 20 25

<210> 9
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse cyclin A2
 destruction box

<400> 9
 Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met
 1 5 10 15
 Leu Leu

<210> 10
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:GenBank
 AAA83272 and AAA947437 kinase "homologue" domain

<400> 10
 Met Ser Ser Arg Ser Ala Ala Arg Arg Asn Asp Gln Asp Val His Val
 1 5 10 15
 Gly Lys Tyr Lys Leu Leu Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
 20 25 30
 Val Lys Leu Ala Lys His Val Ile Thr Gly His Glu Val Ala Ile Lys
 35 40 45
 Ile Ile Asp Lys Thr Ala Leu Asn Pro Ser Ser Leu Gln Lys Leu Phe
 50 55 60
 Arg Glu Val Lys Ile Met Lys Gln Leu Asp His Pro Asn Ile Val Lys
 65 70 75 80
 Leu Tyr Gln Val Met Glu Thr Glu Gln Thr Leu Tyr Leu Val Leu Glu
 85 90 95
 Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
 100 105 110
 Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
 115 120 125
 Val Gln Tyr Leu His Ser Lys Asn Ile Ile His Arg Asp Leu Lys Ala
 130 135 140
 Glu Asn Leu Leu Leu Asp Gln Asp Met Asn Ile Lys Ile Ala Asp Phe
 145 150 155 160
 Gly Phe Ser Asn Thr Phe Ser Leu Gly Asn Lys Leu Asp Thr Phe Cys
 165 170 175
 Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Ser Gly Lys Lys Tyr
 180 185 190
 Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
 195 200 205
 Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
 210 215 220
 Arg Glu Arg Val Leu Arg
 225 230

<210> 11
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:GenBank
AAF72103/MAPK kinase "homologue" domain

<400> 11

Arg Cys Arg Asn Ser Ile Thr Ser Ala Thr Asp Glu Gln Pro His Ile
1 5 10 15

Gly Asn Tyr Arg Leu Gln Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
20 25 30

Val Lys Leu Ala Arg His Val Leu Thr Gly Arg Glu Val Ala Val Lys
35 40 45

Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser Leu Gln Lys Leu Phe
50 55 60

Arg Glu Val Arg Ile Met Lys Ile Leu Asn His Pro Asn Ile Val Lys
65 70 75 80

Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
85 90 95

Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
100 105 110

Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
115 120 125

Val Gln Tyr Cys His Gln Lys Tyr Ile Val His Arg Asp Leu Lys Ala
130 135 140

Glu Asn Leu Leu Leu Asp Gly Asp Met Asn Ile Lys Ile Ala Asp Phe
145 150 155 160

Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr Phe Cys
165 170 175

Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
180 185 190

Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
195 200 205

Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
210 215 220

Arg Glu Arg Val Leu Arg
225 230

<210> 12

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:GenBank G01025
kinase "homologue" domain

<400> 12
 Ile Arg Gly Arg Asn Ser Ala Thr Ser Ala Asp Glu Gln Pro His Ile
 1 5 10 15
 Gly Asn Tyr Arg Leu Leu Lys Thr Ile Gly Lys Gly Asn Phe Ala Lys
 20 25 30
 Val Lys Leu Ala Arg His Ile Leu Thr Gly Lys Glu Val Ala Val Lys
 35 40 45
 Ile Ile Asp Lys Thr Gln Leu Asn Ser Ser Ser Leu Gln Lys Leu Phe
 50 55 60
 Arg Glu Val Arg Ile Met Lys Val Leu Asn His Pro Asn Ile Val Lys
 65 70 75 80
 Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met Glu
 85 90 95
 Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu Val Ala His Gly Arg
 100 105 110
 Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile Val Ser Ala
 115 120 125
 Val Gln Tyr Cys His Gln Lys Phe Ile Val His Arg Asp Leu Lys Ala
 130 135 140
 Glu Asn Leu Leu Leu Asp Ala Asp Met Asn Ile Lys Ile Ala Asp Phe
 145 150 155 160
 Gly Phe Ser Asn Glu Phe Thr Phe Gly Asn Lys Leu Asp Thr Phe Cys
 165 170 175
 Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly Lys Lys Tyr
 180 185 190
 Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Thr
 195 200 205
 Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln Asn Leu Lys Glu Leu
 210 215 220
 Arg Glu Arg Val Leu Arg
 225 230

<210> 13
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:GenBank P51954
 kinase "homologue" domain

<400> 13
 Met Glu Lys Tyr Val Arg Leu Gln Lys Ile Gly Glu Gly Ser Phe Gly
 1 5 10 15

Lys Ala Val Leu Val Lys Ser Thr Glu Asp Gly Arg His Tyr Val Ile
 20 25 30
 Lys Glu Ile Asn Ile Ser Arg Met Ser Asp Lys Glu Arg Gln Glu Ser
 35 40 45
 Arg Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val
 50 55 60
 Gln Tyr Lys Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met
 65 70 75 80
 Asp Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys
 85 90 95
 Gly Ala Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile
 100 105 110
 Cys Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp
 115 120 125
 Ile Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu
 130 135 140
 Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala
 145 150 155 160
 Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu
 165 170 175
 Asn Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val
 180 185 190
 Leu Tyr Glu Leu Cys Thr Leu Lys His Ala Phe Glu Ala Gly Asn Met
 195 200 205
 Lys Asn Leu Val Leu Lys Ile Ile Ser
 210 215

<210> 14

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mkinase kinase
 "homologue" domain

<400> 14

Met Trp Phe Phe Ala Arg Asp Pro Val Arg Asp Phe Pro Phe Glu Leu
 1 5 10 15
 Ile Pro Glu Pro Pro Glu Gly Gly Leu Pro Gly Pro Trp Ala Leu His
 20 25 30
 Arg Gly Arg Lys Lys Ala Thr Gly Ser Pro Val Ser Ile Phe Val Tyr
 35 40 45
 Asp Val Lys Pro Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Ala
 50 55 60

Phe Lys Arg Phe Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile
 65 70 75 80
 Asp Gly Leu Glu Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val
 85 90 95
 Thr Pro Leu Gly Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Gly Leu
 100 105 110
 Lys Glu Leu Glu Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu
 115 120 125
 Ser Phe Leu Val Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met
 130 135 140
 Ala Ala Val Phe Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu
 145 150 155 160
 Asp Tyr Met Tyr Ser Ala Gln Gly Asn Gly Gly Gly Pro Pro Arg Lys
 165 170 175
 Gly Ile Pro Glu Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser
 180 185 190
 Ser Gly Arg Val Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu
 195 200 205
 Gly Cys Leu Ile Trp Glu Val Phe Asn Gly Pro Leu Pro Arg Ala Ala
 210 215 220
 Ala Leu Arg Asn Pro Gly Lys Ile Pro
 225 230

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:kinase
 "homologue" domain consensus peptide

<400> 15

Gly Ser Pro Val

1

<210> 16

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:kinase
 "homologue" domain consensus peptide

<400> 16

Asp Arg Ala Gly

1

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:kinase
"homologue" domain consensus peptide

<400> 17
Gly Cys Leu Ile
1

TOWNSEND & TOWNSEND & CREW LLP
2 EMBARCADERO CTR, SAN FRANCISCO, CA 94111

SEQUENCE LISTING

TRAM ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS AND
METHODS OF USE

Appl.: Luo et al.

Atty Docket No.: 021044-004810US

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